

## CLAIMS

We claim:

1. A method for generating a secondary library of scaffold protein sequences comprising:
  - a) generating a probability distribution table of amino acid residues in a plurality of  
5 variant positions from a force field calculation; and
  - b) combining a plurality of said amino acid residues to generate a secondary library of  
secondary sequences; wherein at least one of said secondary sequences is different from said  
primary sequences.
2. A method according to claim 1 further comprising synthesizing a plurality of said secondary  
10 sequences.
3. A method according to claim 2 wherein said synthesizing is done by multiple PCR with pooled  
oligonucleotides.
4. A method according to 3 wherein said pooled oligonucleotides are added in equimolar  
amounts.
- 15 5. A method according to claim 3 wherein said pooled oligonucleotides are added in amounts  
that correspond to the frequency of the mutation.
6. A method according to claim 3 wherein said pooled oligonucleotides are pooled in relative  
amounts.

20